

Claims

1. A polypeptide variant of TAO1, comprising an amino acid sequence that is at least 80% identical to residues 15-285 of SEQ ID NO:2, with the proviso that the variant does not comprise more than 500 consecutive amino acids of SEQ ID NO:2.
2. A variant according to claim 1, wherein the amino acid sequence is at least 90% identical to residues 15-285 of SEQ ID NO:2.
3. A variant according to claim 1, wherein the variant comprises residues 1-416 of SEQ ID NO:2.
4. A variant according to claim 1, wherein the variant comprises residues 1-320 of SEQ ID NO:2.
5. A variant according to claim 1, wherein the variant comprises residues 15-285 of SEQ ID NO:2.
6. A polypeptide variant of TAO2, comprising an amino acid sequence that is at least 80% identical to residues 15-285 of SEQ ID NO:4, with the proviso that the variant does not comprise more than 500 consecutive amino acids of SEQ ID NO:4.
7. A variant according to claim 6, wherein the amino acid sequence is at least 90% identical to residues 15-285 of SEQ ID NO:4.
8. A variant according to claim 6, wherein the variant comprises residues 1-416 of SEQ ID NO:4.
9. A variant according to claim 6, wherein the variant comprises residues 1-320 of SEQ ID NO:4.

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10. A variant according to claim 6, wherein the variant comprises residues 15-285 of SEQ ID NO:4.

11. A polypeptide variant of ceTAO, comprising an amino acid sequence that is at least 80% identical to residues 47-323 of SEQ ID NO:28, with the proviso that the variant does not comprise more than 500 consecutive amino acids of SEQ ID NO:28.

12. A variant according to claim 11, wherein the amino acid sequence is at least 90% identical to residues 47-323 of SEQ ID NO:28.

13. A variant according to claim 11, wherein the variant comprises residues 1-454 of SEQ ID NO:28.

14. A variant according to claim 11, wherein the variant comprises residues 1-358 of SEQ ID NO:28.

15. A variant according to claim 11, wherein the variant comprises residues 47-323 of SEQ ID NO:28.

16. An isolated polynucleotide encoding a polypeptide according to any one of claims 1-15.

17. An isolated polynucleotide according to claim 16, wherein the polynucleotide comprises at least 800 consecutive nucleotides of SEQ ID NO:1.

18. An isolated polynucleotide according to claim 16, wherein the polynucleotide comprises at least 800 consecutive nucleotides of SEQ ID NO:3.

19. An isolated polynucleotide according to claim 16, wherein the polynucleotide comprises at least 800 consecutive nucleotides of SEQ ID NO:27.

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20. A recombinant expression vector comprising a polynucleotide according to claim 16.

21. A host cell transformed or transfected with an expression vector according to claim 20.

22. A pharmaceutical composition, comprising:

- (a) a variant according to any one of claims 1-15; and
- (b) a physiologically acceptable carrier.

23. A pharmaceutical composition, comprising:

- (a) a polynucleotide according to claim 16; and
- (b) a physiologically acceptable carrier.

24. A method for phosphorylating a MEK polypeptide, comprising contacting a MEK polypeptide with a variant according to any one of claims 1, 6 or 10, wherein the MEK polypeptide comprises MEK3, MEK4 or MEK6 or a variant thereof, and thereby phosphorylating the MEK polypeptide.

25. A method for activating a member of a stress-responsive MAP kinase pathway in an organism, comprising administering to an organism a variant according to any one of claims 1, 6 or 10, and thereby activating a member of a stress-responsive MAP kinase pathway.

26. The method of claim 25 wherein the member of the stress-responsive MAP kinase pathway is MEK3.

27. A method for screening for an agent that modulates signal transduction via a stress-responsive MAP kinase pathway, comprising:

- (a) contacting a candidate agent with a variant according to any one of claims 1, 6 or 10; and

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(b) subsequently measuring the ability of the variant to modulate the activity of a MEK3 polypeptide, and thereby evaluating the ability of the compound to modulate signal transduction via a stress-responsive MAP kinase pathway.

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